RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/016,869B*

INPUT SET: S36811.raw

/600 #34

This Raw Listing contains the General
Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:                    ENTERED
 4
 5      (i) APPLICANT: Beach, David H.
 6                     Demetrick, Douglas J.
 7                     Serrano, Manuel
 8                     Hannon, Gregory J.
 9
10     (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
11            Uses Related Thereto
12
13   (iii) NUMBER OF SEQUENCES: 35
14
15   (iv) CORRESPONDENCE ADDRESS:
16           (A) ADDRESSEE: Ropes & Gray
17           (B) STREET: One International Place
18           (C) CITY: Boston
19           (D) STATE: MA
20           (E) COUNTRY: USA
21           (F) ZIP: 02110
22
23      (v) COMPUTER READABLE FORM:
24           (A) MEDIUM TYPE: Floppy disk
25           (B) COMPUTER: IBM PC compatible
26           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27           (D) SOFTWARE: WordPad
28
29     (vi) CURRENT APPLICATION.DATA:
30           (A) APPLICATION NUMBER: US 09/016,869
31           (B) FILING DATE: 30-JAN-1998
32
33
34    (vii) PRIOR APPLICATION DATA:
35           (A) APPLICATION NUMBER: US 08/893,274
36           (B) FILING DATE: 15-JUL-1994
37
38    (vii) PRIOR APPLICATION DATA:
39           (A) APPLICATION NUMBER: US 08/306,511
40           (B) FILING DATE: 14-SEP-1994
41
42    (vii) PRIOR APPLICATION DATA:
43           (A) APPLICATION NUMBER: US 08/248,812
44           (B) FILING DATE: 25-MAY-1994
45
46    (vii) PRIOR APPLICATION DATA:
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INPUT SET: S36811.raw

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47              (A) APPLICATION NUMBER: US 08/227,371
48              (B) FILING DATE: 14-APR-1994
49
50         (vii) PRIOR APPLICATION DATA:
51              (A) APPLICATION NUMBER: US 08/154,915
52              (B) FILING DATE: 18-NOV-1993
53
54         (vii) PRIOR APPLICATION DATA:
55              (A) APPLICATION NUMBER: US 07/991,997
56              (B) FILING DATE: 17-DEC-1992
57
58        (viii) ATTORNEY/AGENT INFORMATION:
59              (A) NAME: Vincent, Matthew P.
60              (B) REGISTRATION NUMBER: 36,709
61              (C) REFERENCE/DOCKET NUMBER: GPCI-P10-071
62
63          (ix) TELECOMMUNICATION INFORMATION:
64              (A) TELEPHONE: (617) 951-7739
65              (B) TELEFAX: (617) 951-7050
66
67
68     (2) INFORMATION FOR SEQ ID NO:1:
69          (i) SEQUENCE CHARACTERISTICS:
70              (A) LENGTH: 994 base pairs
71              (B) TYPE: nucleic acid
72              (C) STRANDEDNESS: both
73              (D) TOPOLOGY: linear
74
75         (ii) MOLECULE TYPE: cDNA
76         (ix) FEATURE:
77              (A) NAME/KEY: CDS
78              (B) LOCATION: 41..508
79
80         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
81
82  CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATG GAT CCG GCG GCG        55
83                                               Met Asp Pro Ala Ala
84                                               1                   5
85  GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC      103
86  Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala
87                  10                  15                  20
88  CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG      151
89  Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu
90              25                  30                  35
91  CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG      199
92  Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met
93              40                  45                  50
94  ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG      247
95  Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu
96          55                  60                  65
97  CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT      295
98  Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala
99   70                  75                  80                  85
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INPUT SET: S36811.raw

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100   GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG        343
101   Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly
102                     90              95                  100
103   GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG        391
104   Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu
105             105               110               115
106   GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT        439
107   Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
108             120               125               130
109   GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA        487
110   Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu
111             135               140               145
112   GGT CCC TCA GAC ATC CCC GAT TGAAAGAACC AGAGAGGCTC TGAGAAACCT           538
113   Gly Pro Ser Asp Ile Pro Asp
114   150                       155
115   CGGGAAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACTGC CCCCGCCACA      598
116   ACCCACCCCG CTTTCGTAGT TTTCATTTAG AAAATAGAGC TTTTAAAAAT GTCCTGCCTT      658
117   TTAACGTAGA TATAAGCCTT CCCCCACTAC CGTAAATGTC CATTTATATC ATTTTTTATA      718
118   TATTCTTATA AAAATGTAAA AAAGAAAAAC ACCGCTTCTG CCTTTTCACT GTGTTGGAGT      778
119   TTTCTGGAGT GAGCACTCAC GCCCTAAGCG CACATTCATG TGGGCATTTC TTGCGAGCCT      838
120   CGCAGCCTCC GGAAGCTGTC GACTTCATGA CAAGCATTTT GTGAACTAGG GAAGCTCAGG      898
121   GGGGTTACTG GCTTCTCTTG AGTCACACTG CTAGCAAATG GCAGAACCAA AGCTCAAATA      958
122   AAAATAAAAT TATTTTCATT CATTCACTCA AAAAAA                                994
123
124   (2) INFORMATION FOR SEQ ID NO:2:
125
126           (i) SEQUENCE CHARACTERISTICS:
127               (A) LENGTH: 156 amino acids
128               (B) TYPE: amino acid
129               (D) TOPOLOGY: linear
130
131           (ii) MOLECULE TYPE: protein
132
133           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
134
135   Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
136    1               5                   10                  15
137   Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
138                 20                  25                  30
139   Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
140               35                  40                  45
141   Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
142        50                  55                  60
143   Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
144    65                  70                  75                  80
145   Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
146               85                  90                  95
147   Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
148               100                 105                 110
149   Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
150             115                 120                 125
151   Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
152             130                 135                 140
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RAW SEQUENCE LISTING
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153   Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
154   145               150               155
155
156   (2) INFORMATION FOR SEQ ID NO:3:
157
158        (i) SEQUENCE CHARACTERISTICS:
159             (A) LENGTH: 837 base pairs
160             (B) TYPE: nucleic acid
161             (C) STRANDEDNESS: single
162             (D) TOPOLOGY: linear
163        (ii) MOLECULE TYPE: cDNA
164
165        (ix) FEATURE:
166             (A) NAME/KEY: CDS
167             (B) LOCATION: 328..738
168
169        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
170
171   GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG        60
172   CGCTAGGCGC TTTTTCCCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA       120
173   AAAGCCCGGA GCTAACGACC GGCCGCTCGG CACTGCACGG GGCCCCAAGC CGCAGAAGAA       180
174   GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTGCGCCGG       240
175   AGCAGCGTGG GAAAGAAGGG AAGAGTGTCG TTAAGTTTAC GGCCAACGGT GGATTATCCG       300
176   GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG           351
177                                  Met Arg Glu Glu Asn Lys Gly Met
178                                  1               5
179   CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA        399
180   Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly
181    10               15                   20
182   CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC        447
183   Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn
184    25               30                   35                   40
185   GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC        495
186   Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly
187                   45                   50                   55
188   AGC GCC CGC GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG CCC AAC        543
189   Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn
190                   60                   65                   70
191   TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG        591
192   Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg
193                   75                   80                   85
194   GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG GCG CGG        639
195   Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
196                   90                   95                   100
197   CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG        687
198   Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu
199   105               110                  115                  120
200   GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG        735
201   Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly
202                   125                  130                  135
203   GAC TGACGCCAGG TTCCCCAGCC GCCCACAACG ACTTTATTTT CTTACCCAAT            788
204   Asp
205
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INPUT SET: S36811.raw

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206    TTCCCACCCC CACCCACCTA ATTCGATGAA GGCTGCCAAC GGGGAGCGG              837
207
208    (2)  INFORMATION FOR SEQ ID NO:4:
209
210         (i)  SEQUENCE CHARACTERISTICS:
211              (A)  LENGTH: 137 amino acids
212              (B)  TYPE: amino acid
213              (D)  TOPOLOGY: linear
214
215         (ii)  MOLECULE TYPE: protein
216
217         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:4:
218
219    Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu
220     1               5                  10                  15
221    Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
222              20                  25                  30
223    Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
224          35                  40                  45
225    Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu
226        50                  55                  60
227    Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr
228    65                  70                  75                  80
229    Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
230                  85                  90                  95
231    Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
232              100                 105                 110
233    Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala
234          115                 120                 125
235    Gly Tyr Leu Arg Thr Ala Thr Gly Asp
236        130                 135
237
238    (2)  INFORMATION FOR SEQ ID NO:5:
239
240         (i)  SEQUENCE CHARACTERISTICS:
241              (A)  LENGTH: 853 base pairs
242              (B)  TYPE: nucleic acid
243              (C)  STRANDEDNESS: both
244              (D)  TOPOLOGY: linear
245
246         (ii)  MOLECULE TYPE: cDNA
247
248         (ix)  FEATURE:
249              (A)  NAME/KEY: CDS
250              (B)  LOCATION: 213..587
251
252         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:5:
253
254    GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC      60
255
256    GGGCCGCCCA CTCCAAGAGA GGGTTTTCTT GGTGAAGTTC GTGCGATCCC GGAGACCCAG     120
257
258    GACAGCGAGC TGCGCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG     180
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/016,869B*

INPUT SET: S36811.raw

Line	Error	Original Text